

RAW SEQUENCE LISTING

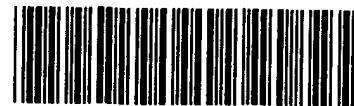
The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/826,157

Source: TFWO

Date Processed by STIC: 10-26-04

ENTERED



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/826,157

DATE: 10/26/2004

TIME: 10:09:35

Input Set : A:\17481-003001.TXT

Output Set: N:\CRF4\10262004\J826157.raw

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4 <110> APPLICANT: Lindquist, Susan L.
5      Outeiro, Tiago
7 <120> TITLE OF INVENTION: YEAST ECTOPICALLY EXPRESSING ABNORMALLY
8      PROCESSED PROTEINS AND USES THEREFOR
10 <130> FILE REFERENCE: 17481-003001
12 <140> CURRENT APPLICATION NUMBER: US 10/826,157
13 <141> CURRENT FILING DATE: 2004-04-16
15 <150> PRIOR APPLICATION NUMBER: US 60/472,317
16 <151> PRIOR FILING DATE: 2003-05-20
18 <150> PRIOR APPLICATION NUMBER: US 60/463,284
19 <151> PRIOR FILING DATE: 2003-04-16
21 <160> NUMBER OF SEQ ID NOS: 8
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 423
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
30 <400> SEQUENCE: 1
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32 aaaaccaaac aggggtgtggc agaagcagca ggaaagacaa aagaggggtgt tctctatgta      120
33 ggctccaaaa ccaaggagggt agtgggtgcat ggtgtggcaa cagtggctga gaagacaaaa      180
34 gagcaagtga caaatgttgg aggagcagtg gtgacgggtg tgacagcagt agcccagaag      240
35 acagtggagg gagcagggag cattgcagca gccactggct ttgtcaaaaa ggaccagttg      300
36 ggcaagaatg aagaaggagc cccacaggaa ggaattcttg aagatatgcc tgtggatcct      360
37 gacaatgagg cttatgaaat gccttctgag gaagggatc aagactacga acctgaagcc      420
38 taa                                                                                   423
40 <210> SEQ ID NO: 2
41 <211> LENGTH: 140
42 <212> TYPE: PRT
43 <213> ORGANISM: Homo sapiens
45 <400> SEQUENCE: 2
46 Met Asp Val Phe Met Lys Gly Leu Ser Lys Ala Lys Glu Gly Val Val
47 1          5          10          15
48 Ala Ala Ala Glu Lys Thr Lys Gln Gly Val Ala Glu Ala Ala Gly Lys
49          20          25          30
50 Thr Lys Glu Gly Val Leu Tyr Val Gly Ser Lys Thr Lys Glu Gly Val
51          35          40          45
52 Val His Gly Val Ala Thr Val Ala Glu Lys Thr Lys Glu Gln Val Thr
53          50          55          60
54 Asn Val Gly Gly Ala Val Val Thr Gly Val Thr Ala Val Ala Gln Lys
55 65          70          75          80
56 Thr Val Glu Gly Ala Gly Ser Ile Ala Ala Thr Gly Phe Val Lys
57          85          90          95

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58 Lys Asp Gln Leu Gly Lys Asn Glu Glu Gly Ala Pro Gln Glu Gly Ile
59          100          105          110
60 Leu Glu Asp Met Pro Val Asp Pro Asp Asn Glu Ala Tyr Glu Met Pro
61          115          120          125
62 Ser Glu Glu Gly Tyr Gln Asp Tyr Glu Pro Glu Ala
63          130          135          140
65 <210> SEQ ID NO: 3
66 <211> LENGTH: 405
67 <212> TYPE: DNA
68 <213> ORGANISM: Homo sapiens
70 <400> SEQUENCE: 3
71 atggacgtgt tcatgaaggg cctgtccatg gccaaaggagg gcgttgtggc agccgcggag      60
72 aaaaccaagc aggggggtcac cgaggcggcg gagaagacca aggagggcgt cctctacgtc      120
73 ggaagcaaga cccgagaagg tgtggtacaa ggtgtggctt cagtggctga aaaaaccaag      180
74 gaacaggcct cacatctggg aggagctgtg ttctctgggg cagggaacat cgcagcagcc      240
75 acaggactgg tgaagaggga ggaattccct actgatctga agccagagga agtggcccag      300
76 gaagctgctg aagaaccact gattgagccc ctgatggagc cagaagggga gagttatgag      360
77 gaccaccccc aggaggaata tcaggagtat gagccagagg cgtag      405
79 <210> SEQ ID NO: 4
80 <211> LENGTH: 134
81 <212> TYPE: PRT
82 <213> ORGANISM: Homo sapiens
84 <400> SEQUENCE: 4
85 Met Asp Val Phe Met Lys Gly Leu Ser Met Ala Lys Glu Gly Val Val
86 1          5          10          15
87 Ala Ala Ala Glu Lys Thr Lys Gln Gly Val Thr Glu Ala Ala Glu Lys
88          20          25          30
89 Thr Lys Glu Gly Val Leu Tyr Val Gly Ser Lys Thr Arg Glu Gly Val
90          35          40          45
91 Val Gln Gly Val Ala Ser Val Ala Glu Lys Thr Lys Glu Gln Ala Ser
92          50          55          60
93 His Leu Gly Gly Ala Val Phe Ser Gly Ala Gly Asn Ile Ala Ala Ala
94 65          70          75          80
95 Thr Gly Leu Val Lys Arg Glu Glu Phe Pro Thr Asp Leu Lys Pro Glu
96          85          90          95
97 Glu Val Ala Gln Glu Ala Ala Glu Glu Pro Leu Ile Glu Pro Leu Met
98          100          105          110
99 Glu Pro Glu Gly Glu Ser Tyr Glu Asp Pro Pro Gln Glu Glu Tyr Gln
100          115          120          125
101 Glu Tyr Glu Pro Glu Ala
102          130
104 <210> SEQ ID NO: 5
105 <211> LENGTH: 384
106 <212> TYPE: DNA
107 <213> ORGANISM: Homo sapiens
109 <400> SEQUENCE: 5
110 atggatgtct tcaagaaggg cttctccatc gccaaaggagg gcgtgggtggg tgcgggtggaa      60
111 aagaccaagc aggggggtgac ggaagcagct gagaagacca aggaggggggt catgtatgtg      120
112 ggagccaaga ccaaggagaa tgttgtagag agcgtgacct cagtggccga gaagaccaag      180

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113 gagcaggcca acgcggtgag cgaggctgtg gtgagcagcg tcaacactgt ggccaccaag      240
114 accgtggagg aggcggagaa catcgcggtc acctccgggg tggcgcgcaa ggaggacttg      300
115 aggccatctg ccccccaaca ggaggggtgtg gcatccaaag agaaagagga agtggcagag      360
116 gagggcccaga gtgggggaga ctag                                           384
118 <210> SEQ ID NO: 6
119 <211> LENGTH: 127
120 <212> TYPE: PRT
121 <213> ORGANISM: Homo sapiens
123 <400> SEQUENCE: 6
124 Met Asp Val Phe Lys Lys Gly Phe Ser Ile Ala Lys Glu Gly Val Val
125 1 5 10 15
126 Gly Ala Val Glu Lys Thr Lys Gln Gly Val Thr Glu Ala Ala Glu Lys
127 20 25 30
128 Thr Lys Glu Gly Val Met Tyr Val Gly Ala Lys Thr Lys Glu Asn Val
129 35 40 45
130 Val Gln Ser Val Thr Ser Val Ala Glu Lys Thr Lys Glu Gln Ala Asn
131 50 55 60
132 Ala Val Ser Glu Ala Val Val Ser Ser Val Asn Thr Val Ala Thr Lys
133 65 70 75 80
134 Thr Val Glu Glu Ala Glu Asn Ile Ala Val Thr Ser Gly Val Val Arg
135 85 90 95
136 Lys Glu Asp Leu Arg Pro Ser Ala Pro Gln Gln Glu Gly Val Ala Ser
137 100 105 110
138 Lys Glu Lys Glu Glu Val Ala Glu Glu Ala Gln Ser Gly Gly Asp
139 115 120 125
141 <210> SEQ ID NO: 7
142 <211> LENGTH: 28
143 <212> TYPE: DNA
144 <213> ORGANISM: Artificial Sequence
146 <220> FEATURE:
147 <223> OTHER INFORMATION: primer
149 <400> SEQUENCE: 7
150 ggactagtat ggatgtattc atgaaagg      28
152 <210> SEQ ID NO: 8
153 <211> LENGTH: 34
154 <212> TYPE: DNA
155 <213> ORGANISM: Artificial Sequence
157 <220> FEATURE:
158 <223> OTHER INFORMATION: primer
160 <400> SEQUENCE: 8
161 ggggaagctt ttattaggct tcaggttcgt agtc      34

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VERIFICATION SUMMARY

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